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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-050-603A-14 - 99.50 147...
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-050-603A-14 - 99.50 147...
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/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-617A-3 + 97.00 128...
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-022-617A-3 + 97.00 128...
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-320-878-22 + 95.50 147...
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-320-878-22 + 95.50 143...
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Query: US-08-978-217-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database sequences: 324599
Database length: 94655562
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-343-443B-3 + 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-691B-43
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-Q-/cgn2_1/USPT0_spco1/US08978217/runat_21092001_160327_2870/app_query.fasta_1.1083
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-USER-US08978217_@CGN1_1_85 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
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                                                                     :US-08-279-996-1
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13-6 + 435.50 799.23 6.7e-37
13-10 + 435.50 799.89 7.0e-37
13-10 + 435.50 417.66 1.2e-15
81-1 + 238.50 416.64 1.4e-15
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alignment_scores:
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/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-328-809-3 +
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                                                                                                                                                                                                                  Align seg 1/1 to: US-08-746-789A-1 from: 1
                                                                                                                                                                                                                                                      US-08-978-217-16 x US-08-746-789A-1
                                                                                                                                                                                                                                                                                                           Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 610 270 4026 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEVENCE ADDRESS:
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
ADDRESSEE: Swedeland Road, P.O. Box 1539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: AT TELECOMMUNICATION INFORMATION: 510 270 5219
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NAME: William T. Han
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM 486
OPERATING SYSTEM: WINDOW:
SOFTWARE: MICROSOFT WORD
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 19406-0939
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                  hrPheGlyThrGluAspLeuValLeuThrLeuAsnAsnGlnGlnMetThr 49
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Ratio: 4.850
milarity: 94.892
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DEDNESS: Single
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                                              333 etArgTyrTyrTyrLysArgGluIleLeuGluArgValAspGlyArgArg
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                                                                                        yGlnLysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaM
                                                                                                                                                  GAAGGCGTCTTCAAGTTCCTGCGCTCCGAGGCTGTGGCCCCAACTATGGGG
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alignment_block:
US-08-978-217-16 x US-09-009-913-2
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; TOPOLOGY: lin
; MOLECULE TYPE:
US-09-009-913-2
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                                                                                                                                                                          Align seg 1/1 to: US-09-009-913-2
                                                                                                                                                                                                                                                        Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
LENGTH: 5427 base pairs
TYPE: nucleic acid
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NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: AxyS Pharmaceuticals, TITLE OF INVENTION: Asthma Relationumber Of SEQUENCES: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEO for Windows
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
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                                              134 TTAGGTA .....
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CLASSIFICATION:
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TELEFAX: 650-327-3231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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317 lnLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaMet 333
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                                                                                                             ysHisAlaProArgGlyThrHisLeuTrpGluPheIleArgAspIleLeu 283
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; TOPOLOGY: 1i; MOLECULE TYPE: US-09-009-913-3
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                                                                                                                                                                                    alignment_block:
                                                                                                                                                                                                                    Percent Similarity:
                                                                                                                                 Align seg 1/1 to: US-09-009-913-3
                                                                                                                                                                    US-08-978-217-16 x US-09-009-913-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for CURRENT APPLICATION NUMBER: US
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TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
406 GCTCCAGCACCTCCTGGACACCAACCAGCTGGATGCCAATTGTATCCCTT 455
                     74 pIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspP 91
                                                                                               58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTr
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ZIP: 943
                                                                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 650-327-3231
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Diskette COMPUTER: IBM Compatik
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
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                                                                 TGGCATGAAATTCATCCTCAGTACTGGACCAAGTACCAGGTGTGGGAGTG
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ve, Suite 2
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seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-009-913-4
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                                         CTGGTATATAAATTTGGGAAGAATGCCCGAGGATGGAGAAAATGAA 1129
                                                               LeuValTyrLysPheGlyLysAsnSerSerGlyTrpLysGluGluGlu 365
                                                                                                                                           etArgTyrTyrTyrLysArgGluIleLeuGluArgValAspGlyArgArg 349
                                                                                                                                                                                                   yGlnLysLysLysAsnSerAsnMetThrTyrGluLysLeuSerArgAlaM 333
                                                                                                                                                                                                                                                                                                 GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGl 316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              rLysH1salaProArgGlyThrHisLeuTrpGluPheIleArgAspIleL 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                       . AAGCACAACCCGAGAGGGACTCACTTATGGGAATTCATCCGCGACATCC
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seq_documentation_block:
; Sequence 4, Application US/09009913
patent No. 6087485

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-alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-978-217-16 x US-09-009-913-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                           74 pIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspP 91
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ZIP: 94301
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CITY: Palo Alto
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leIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSerLeuGly
                                  GCAGCATCTGAAGTGGAACGGCCAGTGCAGTAGTGAC.....
                                                                   uArgAspLeuThrSerAsn.....SerSerAspGluLeuSerTrpI 138
                                                                                                           GAGTTCACCCGGGCGGCAGGGACGGCGGGGCAGCTCCTCTACAGCAACTT
                                                                                                                                                                                    TCCAAGAGTTCGACATCAACGGCGAGCACCTCTGCAGCATGAGTTTGCAG
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seq_documentation_block:
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                                                                                                                                                                                                                     Sequence 338, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
APPLICANT: AXYS Pharmaceuticals,
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                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                  APPLICANT: AxyS Pharmaceuticals, Inc. TITLE OF INVENTION: Asthma Related Genes
                                                                                                                                                                                                                                                                                                                                                                                 350 LeuValTyrLysPheGlyLysAsnSerSerGlyTrpLysGluGluGlu 365
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                                                                                         STREET: 285 Ham.
CITY: Palo Alto
STATE: CA
                                                     COUNTRY: UZIP: 94301
                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GluGlyValPheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGl 316
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USA
                                                                                                                           285 Hamilton Ave, Suite
IBM Compatible
                                                                                                                                              Bozicevic & Reed, LLP
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; LOCATION: 1...848
; OTHER INFORMATION:
US-09-009-913-338
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US-08-978-217-16 x US-09-009-913-338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
                                                                                                                                                                                                                                                                                   122 aGlnLeuArgAspLeuThrSerAsn.....SerSerAspGluLeuS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       168 GGAATGGCTGCAGCACCTCCTGGACACCAACCAGCTAGACGCTAGCTGCA
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                318 CAACCTACAGCATCTCAAGTGGAACGGCCAATGCAGCAGTGAC.....
                                                                                                                                                                                                                                                                                                                                                                         106 LeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLeuHisAl 122
                                                                                                                                                                                                                                                                                                                                                                                                                      218 TCCCTTTCCAGGAGTTCGACATTAGCGGAGAACACCTGTGCAGCATGAGT
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                                                                                                                                                                                                        136 erTrpIleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
                                                                                                                                                                                                                                                                                                                                    268 CTGCAGGAGTTCACGAGGGCAGCAGGCTCAGCTGGGCAGCTGCTCTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                 169 uLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGlyP
                                                                                                                                                                                                                                                                                                                                                                                                                                                89 leAspPheSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAla 105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72 uGluTrpIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 AlaSerTrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 848 base pairs
                                                                                                                                                        .....CTTTTCCAGTCCGCA
CATGAACACATGGAAAGAAGAAACTATCTCTATGATCCCAGCTATGGTA
                                                                               CACAATGTCATTGTCAAGACTGAACAAACCGATCCT
                                                                                                                       LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLe
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Ratio:
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2.864
59.797
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seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-009-913-8
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Sequence 8, Application US/09009913
Patent No. 6087485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEG for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,913
FILING DATE: 21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
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ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-4P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Bozicevic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCES: 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               303 PheLysPheLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLy 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           659
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          253 LeuSerLysGluTyrTrpAspCysLeuGluGlyLysLysSerLysHisAl 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      236 ysLysGlyGluProLysHisGlyLysArgLysArgGlyArgProArgLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          219
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                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                       COMPUTER: IBM CON
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Palo Alto
STATE: CA
                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET:
                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTACAAACGAGAAATCCTGGAACGTGTGGATGGACGA 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     yrTyrLysArgGluIleLeuGluArgValAspGlyArg 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 roGluLeuAsnGluGlyLeuMetLysTrpGluAsnArgHisGluGlyVal 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCAAGAGGCACTCACTTATGGGAGTTCATCCGAGACATTCTCTTGAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGACAACCTCCAGTCAC.....CT
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                                                                                                                                                                                                                                                                                                                                                                                                                                285 Hamilton Ave,
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                                                                                                                                                                                                                                                                                     IBM Compatible
                                                                                                                                                                                                                                                                                                            Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                  & Reed, LLP
Ave, Suite
                                                                                                                                                                                                                                                                                                                                                                                                                                  200
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alignment_block:
US-08-978-217-16 x US-09-009-913-8
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; MOLECULE TYPE:
US-09-009-913-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   141 euLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGly 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      108
258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHi ::: |||::: ::: :::::::||
                                                                                                                                                                                         224
                                                                                                                                                                                                                                                                          208 HisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSe 224
                                                                                                                                                                                                                                                                                                                                                                                                       451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 206 TGGACATCAGTCCACCCTGAATACTGGACTAAGCGCCATGTGTGGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   124 uArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIleGluL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91 heSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGlu 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74 pIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 2280 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX:
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TELEFAX: 650-327-3231
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                                                                                                                                                                                       rLysValPheProArgAspAspPheThrAspTyrLysLysGlyGluProL 241
                                                                                                                                                                                                                                 AAGACTATGCTGATTCCAACTGCTTGAAAACAAGTGGCATCAAAAGTCAA 520
                                                                                                                                                                                                                                                                                                                                                             roGlySerSerAspValSerThrAlaArgThrAlaThrProGlnSerSer 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyAr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .....TTCATCCTCCAGA 410
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2.623
53.722
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Percent Identity:
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/09009913
Patent No. 6087485
GENERAL INFORMATION:
                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
REFERENCE/DOCKET NUMBER: SEQ-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     612
                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 2428 base pairs
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 21-JAN-19
                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: AxyS Pharmaceuticals, Inc.
TITLE OF INVENTION: Asthma Related Genes
NUMBER OF SEQUENCE: 339
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            809
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                              TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Palo Alto
                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerSerGlyTrpLysGluGluGluVal 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACACGGGTGGCAGGAAGACAAGCTA 835
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGluAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMe 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TCTATGGGAATTTGTACGAGACCTGCTTCTATCTCCTGAAGAAAACTGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Bozicevic & Reed, LLP
285 Hamilton Ave, Suite 200
                                                                                                                                            650-327-3231
                                                                                                                                                                                                                                                                                                                      21-JAN-1998
                                                                                                                                                                                                                                                                                                                                      US/09/009,913
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                                                                                                                                                                                          SEQ-4P
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alignment_scores:

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alignment_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 141 euLeuGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGly 157
291 lyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArg
                                                                                                                                                                              710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             619 AAGACTATGCTGATTCCAACTGCTTGAAAACAAGTGGCATCAAAAGTCAA 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          124 uArgAspLeuThrSerAsnSerSerAspGluLeuSerTrpIleIleGluL 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          354 TGGACATCAGTCCACCCTGAATACTGGACTAAGCGCCATGTGTGGGAGTG
                                                                                                                                                                                                   274 sLeuTrpGluPheIleArgAspIleLeuIleHisProGluLeuAsnGluG
                                                                                                                                                                                                                                                                 669 ...GACTGT.....CACAGTCATAGTAGAACAAGCCTCCAAAGTTCTCA
                                                                                                                                                                                                                                                                                                           258 TrpAspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThrHi
                                                                                                                                                                                                                                                                                                                                                                                                241 ysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluTyr 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              208 HisAlaSerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSe 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              158 ProPheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyAr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          559 ACATCCGCACAAGGTTACTCCTTT............
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      504 GAGTTCGTCGAGGCAGCTGGCCTCTGCGGCGAGTACCTGTAC.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 TCTGCAACTTCAACATCAGTGGCCTGCAGCTGTGCAGCATGACACAGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 rLysValPheProArgAspAspPheThrAspTyrLysLysGlyGluProL 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91 heSerArgCysAsnMetAspGlyAlaThrLeuCysSerCysAlaLeuGlu
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                                                                                     GCATTCTGGAATGGGAAGATAGGGAACAAGGAATTTTTCGGGTGGTTAAA
                                                                                                                                                                            TCTATGGGAATTTGTACGAGACCTGCTTCTATCTCCTGAAGAAAACTGTG
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Gaps: 6
Percent Identity: 30.744
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alignment_block:
US-08-978-217-16 x US-09-009-913-10
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                                                                                                        Align seg 1/1 to: US-09-009-913-10
                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 2498 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10,
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TITLE OF INVENTION: Asthma Related Genes
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                                  423 TGGACATCAGTCCACCCTGAATACTGGACTAAGCGCCCATGTGTGGGAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: SE
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-327-3231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
OPERATING SYSTEM: DO
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        910
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                        58 TrpThrSerGluArgProGlnPheTrpSerLysThrGlnValLeuGluTr
74 pIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 200 ....
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Sherwood, Pamela J
REGISTRATION NUMBER: 36,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/0 FILING DATE: 21-JAN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U
ZIP: 94301
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 650-327-323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
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                                                                                                                                                                                                                              Quality:
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6087485
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285 Hamilton Ave,
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Ave, Suite
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                                                                                                                                                                                             Percent Identity:
                                                                                                        from: 1 to: 2498
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                                                                                                                          341 leLeuGluArgValAspGlyArgArgLeuValTyrLysPheGlyLysAsn 357
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                                                                                                                                                                                                                                                                                                 SerGluAlaValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMe 324
|||||||||:::|||::::||
TCGGAAGCCCTGGCAAAGATGTGGGGACAAAGGAAAAATGACAGAAT 928
                          SerSerGlyTrpLysGluGluGluVal 366
                                                                                                                                                                                                                                                                                                                                                                                                                              lyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPheLeuArg
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GCACACGGGTGGCAGGAAGACAAGCTA 1052
                                                                                                  TTTTGGAGCGGGTTGAC...CGAAGGTTAGTGTACAAATTTGGAAAAAAT
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-368-281-1

seq_documentation_block:

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; MOLECULE TYPE: US-08-368-281-1
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us-08-978-217-16 x us-08-368-281-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: US-08-368-281-1 from: 1 to:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
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Patent No.
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                                                                                                                   494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19400
COMPUTER REALDABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
                                         509
                                                                                                                                                       245
                                                                                                                                                                                                                                228
                                                                                                                                                                                                                                                                      394 ATCACCAGATAGCCATGAACCAATGAAAAAGAAAAAAGTTGGCCGTAAAC 443
                                                                                                                                                                                                                                                                                                                                                344 GAGGTGTCAACTGAAGAGTCTGAACCCATGGATACCTCTCCTATTCCAAC
                                                                                                                                                                                                                                                                                                                                                                                  195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAs
                                                                               261
                                                                                                                                                                                                                                                                                                        211 pSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysValPheP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Oettgen, Joerg P
APPLICANT: Kunsch, Charles A
278 helleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/368,281 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                         uGluGlyLysLysSerLysHisAlaProArgGlyThrHisLeuTrpGluP 278
                                                                                                             AAGAAGAAACCAAGA.....
                                                                                                                                                   ArgLysArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLe
                                                                                                                                                                                           CAAAGACCCAGCAATCACCAATTTCCAATGGGTCTCCTGAGTTAGGTATA 493
                                                                                                                                                                                                                            roArgAspAspPheThrAspTyrLysLysGlyGluProLysHisGlyLys
                                     .GAAGGAAAAGGAAACACA......ACCTATTTGTGGGAGT
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5. 5721113
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61.250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity:
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alignment_block:
US-08-978-217-16 x US-08-368-281-3
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                                    Align seg 1/1 to: US-08-368-281-3
                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08368281 Patent No. 5721113
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APPLICANT: Liberm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Kunsch, Charles A
TITLE OF INVENTION: NERF Genes
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195 AspValSerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAs 211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
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                                                                                                                                                            Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                             nucleic acid
DEDNESS: double
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: USA
                                                                                                                                                                                                                                                                                                                                                                    3240 base pairs
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                                                                                                                                         238.50
2.434
61.250
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                                                                                                                                         Percent Identity: 33.750
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seq_documentation_block:
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ATTORNEY/AGENT INFORMATION:
NAME: MONACO, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 833
TELECOMMUNICATION INFORMATION:
                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                              SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda
STREET: Two Penn Center,
CITY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Calabretta, Bruno
APPLICANT: Skorski, Tomasz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      958 CCATGGGACGAGCTTTGAGATACTACCAAAGGGGAATTCTTGCAAAG 1007
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                                                                                                           FILING DATE:
                                                                                                                                                                         APPLICATION NUMBER: US/08/306,6 FILING DATE: September 15, 1994 CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                ZIP: 19102
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OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
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enter, Suite 1800
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: US-08-306-691B-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-978-217-16 x US-08-306-6918-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: NO. 5734039e INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                       153 LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLe 169
                                                                                                                                                                                                                                                                                                                                                         655
                                                                                                                                                                                                                                                                                                                                                                                                  137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120 uHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          104 CysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLe 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      418 AAGCATTAAAAGCTACTTTCAGTGGTTTCACTAAAGAACAGCAACGACTG 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 .....CTATTAACTCCAAGCAGCAAAGAAATGATGTCTC 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          345 CTTTTCCCCCCCGGATATGGAATGTGCAGATGTCCCA.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                         169 uLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGly. 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        74 pIleSerTyrGlnValGluLysAsnLysTyrAspAlaSerSerIleAspP 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 heSerArgCysAsnMetAspGlyAlaThrLeuCysSer ..... 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 luGlyProGluLys......62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 eGlyThrGluAspLeuValLeuThrLeuAsnAsnGlnGlnMetThrLeuG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 MetTyrSerSerGluAspProThrLeuAlaProAlaProProThrThrPh 34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1604 base pairs
                                                                                                                                                                                                                                                                                                                                                  GGGAACATCTAGAGATCCTGCAGAAAGAG......683
  ATCACAGAGTCCTATCAGACGCTCCATCCCATCAGCTCGGAAGAGCTCCT
                                      TTGAGCATGCCCAGTGTTCCCACCATCGGAGTTCTCAGAGCCCAGCTTC
                                                                                                                                ProGlyAlaProSer.....
                                                                                                                                                                           CTATCCAGAATCCCGCTATACCTCGGATTACTTCATTAGC...TATGGTA 768
                                                                                                                                                                                                                                                                  .....GATGTGAAACCATATCAAGTTAATGGA.....GTCAACCCAGC 721
                                                                                                                                                                                                                                                                                                                                                                                            rp...IleIleGluLeuGluLysAspGlyMetSerPheGlnGluSer 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGCTTTCTCGAG..... 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTGATGTGGGCTGTG.....AATGAATTCAGCCTGAAAGGTGTAGACT 561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
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(215) 568-5549
                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CTGGCCCCAGACTTTGTTGGGGACATCTTAT 654
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. 25
. 22.609
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868

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seq_documentation_block:
Sequence 9, Application PC/TUS9306251
GENERAL INFORMATION:
APPLICANT: Wickstrom, Eric and Rife, Jason P.
TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing
TITLE OF INVENTION: Stereospecific Alkylphosphonates and Arylphosphonates
UNMBER OF SEQUENCES: 93
                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US93-06251-9
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                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    344 rgValAspGlyArgArgLeuValTyrLysPheGly......LysAsn 357 ::::: |||:::||| ||||||:::|||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   327 uLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGluIleLeuGluA 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         210
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                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       oLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluT 257
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                                                                                                                                                                                                                                                                                                                                       CTGCTGGGGTACACCCCTGAGGAGCTG 1565
                                                                                                                                                                                                                                                                                                                                                                                    SerSerGlyTrpLysGluGluGluVal 366
                                                                                                                                                                                                                                                                                                                                                                                                                                         AGACAGCGGGGAAACGCTACGTGTACCGCTTTGTGTGTGACCTGCAGAGC 1538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAACTGAGCCGTGGCCTACGCTACTATTACGACAAAAACATCATCCACA 1488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGGCCAGGAGATGGGGAAAAGAGGAAAAACAAACCTAAGATGAATTATGA 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCTTCTGGAATTACTCACTGATAAATCCTGT...CAGTCTTTTATCAGCT 1344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCCCTAGCTGGCTACACAGGCAGTGGACCAATCCAGCTATGGCAGTT 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATGTGCGGGACCGTGCTGACCTCAATAAGGACAAGCCTGTCATTCCTGCT 1247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTCCCTCCTATGACAGCTTCGACTCAGAGGACTATCCGGCTGCCCTGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCACCCAGTCCTGGAGCAGCCAGTCATCTTTCA...ACAGCCTGCAGCGT 1115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVa 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGCCAGGACTCTTTTGAAAGCATAGAGAGCTACGATAGTTGTGATCGCC 1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTCACCCCAGACAACATGTGCATGGGGAGGACCAGTCGTGGTAAACTCGG 1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .....Ala 209
E: SCULLY, SCOTT, MURPHY & PRESSER 400 Garden City Plaza
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US-08-978-217-16 x PCT-US93-06251-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; STRANDEDNESS: dou
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
PCT-US93-06251-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: DIGIGILIO, Frank S.
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 8586
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
TELEFAX: 516-742-4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                               418 AAGCATTAAAAGCTACTTTCAGTGGTTTCACTAAAGAACAGCAACGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     345 CTTTTCCCCTCCCGGATATGGAATGTGCAGATGTCCCA......
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                                                                                                                                                                            104 CysAlaLeuGluGluLeuArgLeuValPheGlyProLeuGlyAspGlnLe 120
                                                                       120 uHisAlaGlnLeuArgAspLeuThrSerAsnSerSerAspGluLeuSerT
                                                                                                                                                                                                                                                                               91 heSerArgCysAsnMetAspGlyAlaThrLeuCysSer.....
                                                                                                                                                                                                                                                                                                                                                                 51 luGlyProGluLys.....AlaSerTrpThrSerGluArg.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                               TGCTTTCTCGAG
                                                                                                                                                                                                                                                                                                                                    GGTGATGTGGGCTGTG.....AATGAATTCAGCCTGAAAGGTGTAGACT
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46.304
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                             .CTGGCCCCAGACTTTGTTGGGGACATCTTAT
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Percent Identity:
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22.609
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561 91 517 74 467 62 417 51 383 34

611

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1198
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344 rgValAspGlyArgArgLeuValTyrLysPheGly.....LysAsn 357
                                                                                                                                                                                                                      311 ValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetThrTyrGl 327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      257 yr...TrpAspCysLeuGluGlyLysLysSerLys......
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240 oLysHisGlyLysArgLysArgGlyArgProArgLysLeuSerLysGluT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               919 TCCAGACAGACCTTGCAGAATGACTACTTTGCTATCAAACAAGAAGTC 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186 ProGlyAlaProSer.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        169
                                                        GAAACTGAGCCGTGGCCTACGCTACTATTACGACAAAAACATCATCCACA 1488
                                                                                                        uLysLeuSerArgAlaMetArgTyrTyrTyrLysArgGluIleLeuGluA 344
                                                                                                                                                                                                                                                                                                                                                                                                                                          eIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMetLysT 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCTGCCCTAGCTGGCTACACAGGCAGTGGACCAATCCAGCTATGGCAGTT 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTGCGGGACCGTGCTGACCTCAATAAGGACAAGCCTGTCATTCCTGCT 1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lPhePro..ArgAspAspPhe.....ThrAspTyrLysLysGlyGluPr 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTCCCTCAAGTATGAGAATGACTACCCCTCGGTCATTCTCCGAGACCCTC 918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  uLeuAspAspGlyArgGlnAlaSerProTyrTyrCysSerThrTyrGly. 185
                                                                                                                                                                                                                                                                            GGACAGGA.....GATGGCTGGGAATTCAAACTTTCTGACCCAGATGAG 1388
                                                                                                                                                                                                                                                                                                                               rpGluAsnArgHisGluGly...ValPheLysPheLeuArgSerGluAla 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SerAspSerGlyGlySerAspValAspLeuAspLeuThrGluSerLysVa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spValSerThrAlaArgThrAlaThrProGlnSerSerHis.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATCCAGAATCCCGCTATACCTCGGATTACTTCATTAGC...TATGGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LeuGlyAspLeuGlyProPheAspGlnGlySerProPheAlaGlnGluLe
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                                                                                                                                                                                                                                                                                                                                                                                     TCTTCTGGAATTACTCACTGATAAATCCTGT...CAGTCTTTTATCAGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       rp...IleIleGluLeuLeuGluLysAspGlyMetSerPheGlnGluSer 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . AAGCCCAAGGGCACCTTCAAGGACT 1197
                                                                                                                                                                    1438
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698 195 819 191 769 722

684 153 137

1345

295

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alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-343-443B-3
    Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: AEDIT 1.0 DOS text editor
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/343,443B
FILING DATE: 18-NOV-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR93/00494
FILING DATE: 19-MAY-1993
PRIOR APPLICATION DATA:
ADDITICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                          TELEFAX: 215-875-8394
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: ZUCMAN, JESSÍCA
TITLE OF INVENTION: NUCLEIC
TITLE OF INVENTION: CHROMOSC
TITLE OF INVENTION: TRANSLAT
TITLE OF INVENTION: TRANSLOC
TITLE OF INVENTION: TRANSLOC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1489 AGACAGCGGGAAACGCTACGTGTACCGCTTTGTGTGTGACCTGCAGAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: 215-875-8383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             358 SerSerGlyTrpLysGluGluGluVal 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 20-MAY-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 230 CONTROL OF CTTY: Philadelphia
                                                                                                                                                                                                                                                                                                                                                                                     NAME: Weiser, Gerard J.
REGISTRATION NUMBER: 19
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY: UZIP: 19102
                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                               NAME/KEY:
                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                              LOCATION:
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                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION:
                                                                                                                                                                                                                                           nucleic acid
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230 South Fifteenth Street
                                                                                                                                                                                                                                                                                                                               215-875-8394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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Desmaze, Chantal
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Ploougastel, Beatrice
Thomas, Gilles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Melot, Thomas
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                                                                                                                                            143..1498
                                                                                                                                                               CDS
                                                                                                                                                                                                       linear
225.00
1.243
49.454
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FR 92/06123
                                                                                                                                                                                                                                                                                                            ω
    Percent Identity:
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  366
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24.590
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alignment_block:
US-08-978-217-16 x US-08-343-443B-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147
                                                       258 paspCysLeuGluGlyLysLysSerLysHisAlaProArgGlyThr....
                                                                                                                                                                                                                                                                                                                                                                         794 ....GAAGACCCTTCTTATGACTCAGTCAGAAGAGGAGCATGGGGCAATA 839
                                                                                                                                                                                                                                                                                                                                                                                                                                213 yGlySerAspValAspLeuAspLeuThrGluSerLysValPheProArgA 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           197 SerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerG1 213
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758 ......TCCCACACCGACCAATCCTCACGATTGACTGTCAAA.. 793
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                163 rProPheAlaGlnGluLeuLeuAspAspGlyArgGlnAlaSerProTyrT 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             113 eGlyProLeuGlyAspGlnLeuHisAlaGlnLeuArgAspLeuThrSerA 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       629 GATGGCAAGGAACTGTGTAAAATGAACAAGGAGGACTTC.....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      584 .....GAGTATAGCTTGATGGAGATCGACATCCTTTTTCCAGAACATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            385 GGACTGCAGCGTTAGCAAATGCAGCAAGCTGGTGGGCGGAGGCGAGTCCA 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64 nPheTrpSerLysThrGlnValLeuGluTrpIleSerTyrGlnValGluL 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39 euValLeuThrLeuAsnAsnGlnGlnMetThrLeuGluGlyProGluLys 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25 ......ThrLeuAlaProAlaProThrThrPheGlyThrGluAspL 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9 AsnValPheSerAsnTyrPheAsnAlaMetTyrSerSerGluAspPro...
                                                                                                                           ATCAGTAAGAATACAGAGCAACGGCCCCAG
                                                                                                                                                            .....LysArgLysArgGlyArgProArgLysLeuSerLysGluTyrTr 258
                                                                                                                                                                                                                                                ACATGAATTCTGGCCTCAACAAAAGTCCTCCCCTTGGAGGGGCACAAACG
                                                                                                                                                                                                                                                                                                     spaspPheThraspTyrLysLysGlyGluProLysHisGly.....
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACAACACGGAAGTGCTG.....
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TCAGATCCTGGGCCCGACCAGCAGTCGCCTAGCCAACCCTGGAAGCGGGC 980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 snSerSerAspGluLeuSerTrpIleIleGluLeuLeuGluLysAspGly 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .....CTCCGCGCCACCACCTCT 686
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AspGlyAlaThrLeuCysSerCysAlaLeuGluGluLeuArgLeuValPh 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .....TTGTCACACCTCAGTTACCTCAGGGAAAGTTC 735
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                                                                                                                        .....CCAGATCCGTA 930
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alignment_block: us-08-978-217-16 \times us-09-344-579-1
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; LOCATION: (291)..(1700)
US-09-344-579-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
: LENGTH: 2268
: TYPE: DNA
: ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
Sequence 1, Application US/09344579
: Patent No. 6054316
: GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-344-579-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-09-344-579-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Brenda F. Baker
APPLICANT: Lex M. Cowsert
TITLE OF INVENTION: ANTISENSE MODULATION OF ETS-2 EXPRESSION
FILE REFERENCE: RTS-0063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/344,579 CURRENT FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1175 AAAAACATTATGACCAAAGTGCACGGCAAAAGATATGCTTACAAATTT 1222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       495
                                                                                                                                                                                                                                                                                                                                                                 477
605 GTGGAGTGAGCAACAGGTATGCCAGTGGCTTCTCTGGGCCACC.....A 648
                                                                                       576 CGCCTGGGCATTCCA..
                                                                                                                                                                             528 ..AGTCAAGCCTTAAAAGCTACCTTCAGTGGCTTCAAAAAGGAACAGCGG 575
                     65 eTrpSerLysThrGlnValLeuGluTrpIleSerTyrGlnValGluLysA 82 :||||||::: |||||| :::|||::: ::: ::: |
                                                                                                                                                                                                                       35 lyThrGluAspLeuValLeuThrLeuAsn.....AsnGlnGlnMet 48
                                                                                                                                                                                                                                                                                                               18 tTyrSerSerGluAspProThrLeuAlaProAlaProProThrThrPheG 35
                                                                                                                                                                                                                                                                                                                                                                                    2 AlaAlaThrCysGluIleSerAsnValPheSerAsnTyrPheAsnAlaMe 18
:::|||:::|||||:::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ArgGluIleLeuGluArgValAspGlyArgArgLeuValTyrLysPhe 354
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 eLeuArgSerGluAlaValAlaGlnLeuTrpGlyGlnLysLysLysLysAsnS 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AACGCCAGCTGTATCACCTGGGAGGGGACCAAC...GGGGAGTTCAAAAT 1074
                                                                                                                             ThrLeuGluGlyProGluLysAlaSerTrpThrSerGluArgProGlnPh 65
                                                                                                                                                                                                                                                                    TCCGCCAACTGTGAATTG......494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AsnGluGlyLeuMetLysTrpGluAsnArgHisGluGlyValPheLysPh 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   220.00
0.995
49.220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length: 449
Gaps: 21
Percent Identity: 21.158
                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                       AAGAACCCCTGGCT 604
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6
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320	sPheLeuArgSerGluAlaValAlaGlnLeuT	304
4	narghisGiusiyvale : :: AGACGGATGGGAGT	424
4	ATTCAGCTGTGGCAGTTTCTCCTGGAGCTGCTATCAGACAAATCCT	3/4
88	HisLeuTrpGluPheIleArgAspIleLeuIleHisProGluL	7
1373	GTTATACCTGCAGCTGTGCTGGCCGGCTTCACAGGAAGTGG	332
273	LysHisAlaProArgGlyThr	265
1331	AAACCA	325
265	oArgLysLeuSerLysGluTyrTrpAspCysLeuGluGl 	248
248 1324	ysLysGlyGluProLysH1sGlyLysA :::::::::: AGAGGAGTGACCCAGTG.:	23 4 287
1286	CTGCAGCCAGTCTCTCTGCCTCAATAAGCCAACCATGTCTTTC	237
233	ProArgAspAs	228
Ν	CGTCCTTGCTGGATGTGCAACGGGTTCCTTCCTTCGAGAGCTTCGA	187
N	LeuAspLeuThrGluSerLysValPhe	219
218 1186	TCCCTCCTC	214 137
1	CHARLES TO THE TAXABLE TO COMMENTE TO COMMENT CONTRACT CONTRACTOR	
213	erThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGly ::::::: ::::: TCACCAACAATTCTGGGACTCTCCAAAGACTACTACTACTACTACTACTACTACTACTACTACTACTA	197 087
197 1086	rGlyProGlyAlaProSerProGlySerSe 	181 046
0	GATGTTCCCCAAGTCTCGGCTCAGCTCCGTC	996
181		179
178 995	rgGlnAlaSerPro	171 946
171 945	ProPheAspGlnGlySerProPhe <i>F</i> ::: ATGCAGACACAGAATTACCCC <i>F</i>	15 4 899
154 898	luLysAspGlyMetSerPheGlnGlus::::::::::::::::::::::::::::::::::::	138 849
848	::: 	799
137	SerAspGluLeuSerT	131
131 798	급 드 듀	114 749
748	CTGTGTAACCTTGGCAAGGAACGCTT	699
698	TGAATCTGCAGAGGTTCGGCATGAATG	649
98	snLysTyrAspAlaSerSerIleAspPheSerArgCysAsnMetAspGly	N

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· · Percent Similarity:
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US-08-978-217-16 x US-09-360-779-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (112)..(1131)
US-09-360-779-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-360-779-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-360-779-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Deneris, Evan S.
APPLICANT: Pydooro, Dmitry V.
APPLICANT: Fydooro, Dmitry V.
APPLICANT: Hendricks, Timothy J.
APPLICANT: CASE-03828
TITLE OF INVENTION: Useful in the Treatment of Neurological Diseases
FILE REFERENCE: CASE-03828
FILE REFERENCE: CASE-03828
CURRENT APPLICATION NUMBER: US/09/360,779
CURRENT FILING DATE: 1999-07-26
EARLIER APPLICATION UNMBER: 607/094,264
EARLIER FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1752
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Rattus norvegicus
                                                                                                                                                                                           223
                                                                                                                                                                                                                                                                                                                                                                                                          115 ProLeuGlyAspGlnLeuHisAla.............GlnLeuArgAspLe 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     354 heGly......LysAsnSerSerGlyTrpLysGluGluGluVal 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              337 rLysArgGluIleLeuGluArgValAspGlyArgArgLeuValTyrLysP 354
                                                                                             247
                                                                                                                                                                                                                                                                                 282 GGCCTTGCCGGACCCGGCGGCGTCTACTCTTCCCTGTCACCCACAGTCAC
                                            175 nAlaSerPro......TyrTyrCysSerThrTyrGlyP 186
                                                                                                                                       159 PheAspGlnGlySerProPheAlaGlnGluLeuLeuAspAspGlyArgGl 175
                                                                                                                                                                                                                                  142 euGluLysAspGlyMetSerPheGlnGluSerLeuGlyAspLeuGlyPro 158
                                                                                                                                                                                                                                                                                                                             127 uThrSerAsnSerSerAspGluLeuSer.....TrpIleIleGluLeuL 142
                                                                                                                                                                                                                                                                                                                                                                                    133 CCTCTGGGGGAGAGGGTTCCAGCCCCCCCCACCCCCTCAGCCCCATCCCCT 182
                                                                                                                                                                                      TCGTGTGCGACCTCCAGAACTTGCTGGGGTTCACGCCCGAGGAACTG 1661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CGACAAGAACATCATCCACAAGACGTCGGGGAAGCGCTACGTGTACCGCT 1614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   214.00
1.621
50.575
                                                                                           Length: 261
Gaps: 13
Percent Identity: 29.502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1 to: 1752
                                                                                                281
  331
                                                                                                                                                                                                                                                                                        222
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344 766	716	327	666	310	619	294	572	277	522	263	508	247	482	230	432	213	382	197	332	186
ArgValAspGlyArgArgLeuValTyrLysPhe 354 ::: ::: ::: ::: AAGGTGCACGCCAAGCGCTACGCCTAT 798	::	luLvsLeuSerArgAlaMetArgTvrTvrTvrLvsArgGluTleLeuGlu	::: ::::: :::: ::::: :::: :::: ::::::	aValAlaGlnLeuTrpGlyGlnLysLysLysAsnSerAsnMetThrTyrG	GCGTGGGAGGCGCCACGGCGAGTTCAAGCTCACCGACCCCGACGA	LysTrpGluAsnArgHisGluGlyValPheLysPheLeuArgSerGluAl	AGTTTCTACTGGAGCTGCTGGCAGACCGCGCGAACGCCGGCTGCATC	luPheIleArgAspIleLeuIleHisProGluLeuAsnGluGlyLeuMet	GCCGCTGAGCCCTGCGGTACAGAAAGGCAGCGGGCAGATCCAGTTGTGGC	YLysLysSerLysHisAlaProArgGlyThrHisLeuTrpG	AGCCCGAGCTGG	ArgGlyArgProArgLysLeuSerLysGluTyrTrpAspCysLeuGluGl	GAGATGGTCTTTTAAGGAAGGGAAG	spAspPheThrAspTyrLysLysGlyGluProLysHisGlyLysArgLys	CGGCACCTCCCAGCCCCTGCTGATCAACATGTACCTACCAGATCCCGTCG	yGlySerAspValAspLeuAspLeuThrGluSerLysValPheProArgA	CGGTCCCCCCATCTCCCACCGCCCAGTCCCCGGCAGCGATGAGACAGAG	SerThrAlaArgThrAlaThrProGlnSerSerHisAlaSerAspSerGl	CACGGGCGGGTATCGGCACCCCAAGCGCAAAGCTGACGTGCCCCCCCGTG	roGlyAlaProSerProGlySerSerAspVal
	765	343	715	327	665	310	618	293	571	277	521	263	507	246	481	230	431	213	381	196

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